

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 09:57:30 ; Search time 7349 Seconds  
(without alignment)

11402.551 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataagaag.....ctcttccttcagtgcaag 1772

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
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6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772	100.0	1772	6	AX063520 Sequence
2	1772	100.0	1803	6	AX063522 Sequence
3	1729.8	97.6	168173	8	AP004988 Oryza sat
4	1686	95.1	1686	6	AX063525 Sequence
5	1082.4	61.1	2000	6	AX656635 Sequence
6	103.8	5.9	139653	2	AP005890 Oryza sat
7	103.8	5.9	161865	8	AP005912 Oryza sat
8	99.8	5.6	173770	8	OSJN00076
9	99.2	5.6	88044	8	AC145780
10	99	5.6	159636	8	AC090485
11	98.8	5.6	121202	8	AP004190
12	98.8	5.6	135914	8	AP003883
13	98.2	5.5	134058	8	AC037425 Oryza sat
14	98.2	5.5	300029	8	AE017105 Oryza sat
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19	96	5.4	142772	8	AP004184 Oryza sat

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## ALIGNMENTS

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LOCUS AX063520 1772 bp DNA linear PAT 24-JAN-2001  
DEFINITION Sequence 1 from Patent WO0078975.  
ACCESSION AX063520  
VERSION AX063520.1 GI:12541259  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Donaldson, I.A. and Rasmussen, T.B.  
TITLE Rice sucrose synthase promoter  
JOURNAL Patent: WO 0078975-A 1 28-DEC-2000;  
DANISCO A/S (DK)  
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## ORIGIN

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RESULT 2
AX063522 1803 bp DNA linear PAT 24-JAN-2001
LOCUS Sequence 3 from Patent WO0078975.
DEFINITION AX063522
ACCESSION AX063522
VERSION AX063522.1 GI:12541261
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Donaldson, I.A. and Rasmussen, T.B.
TITLE Rice sucrose synthase promoter
JOURNAL Patent: WO 0078975-A 3 28-DEC-2000;
DANISCO A/S (DK)
FEATURES
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Query Match 100.0%; Score 1772; DB 6; Length 1803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 3

AP004988

LOCUS

DEFINITION

AP004988

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

AP004988 168173 bp DNA linear PLN 22-JUL-2004  
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,  
BAC clone: B1056G08.  
AP004988 GI:24060020  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC  
clone: B1056G08  
Published Only in Database (2002)  
2 (bases 1 to 168173)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Submitted (27-MAR-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kamondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,  
Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
On Oct 16, 2002 this sequence version replaced gi:22212589.  
Genes were predicted from the integrated results of the following:  
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH  
(http://www.softberry.com/), GeneMark.hmm  
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM  
(http://www.tigr.org/tdb/glimmer/glimr form.html), RiceHMM  
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor  
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4  
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2  
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The  
genomic sequence was searched against NCBI NonRedundant Protein  
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA

sequence database at RGP or DBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-', and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of B1056G08 clone has an overlap with P0616D06 (DBJ: AP005198) at 5' end and an overlap with P0552F09 clone (DBJ: AP004308) at 3' end and an overlap with P0560B08 clone (DBJ: AP004309) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/genomeSeq.html>.

#### FEATURES

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1. .168173

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REFERENCE 1  
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,  
Katagiri, F., Qian, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.  
TITLE Plant genes involved in defense against pathogens  
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AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.  
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JOURNAL Published Only in Database (2002)  
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AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.  
TITLE Direct Submission  
JOURNAL Submitted (13-NOV-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
COMMENT NOTE: It currently consists of 1 contigs. Gaps between the contigs  
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KPSDIDPTGKPDQAVTEPNLSDNDEKSDKSPNKLPRKTPMRKLAGROMPKIRTSK
TATTPTGKPDQAVTEPNLSDNDEKSDKSPNKLPRKTPMRKLAGROMPKIRTSK
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LQDSNFGSLGSKGAQTRMAQEKQIEALKKQVLAQORLAKVEDEKTKSQAOQ
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Query Match  
Best Local Similarity 79.8%;  
Matches 130; Conservative 0; Mismatches 32; Indels 1; Gaps 1;



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Db 17213 ACTTTGGATATAAGTAAGTAAGTCACAAGAAAAATAATAATTCRAATTTTAAATA 17154
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Db 17153 AGACAGAGTGCTCAACAGGCTGAAGCAAAATCTCAAAATTCCTTATATATGGGACGGTAT 17094
Qy 120 ATTATGGGACGGAGGAGTGAAGATTCTAGCCCAAGAAAAA 162
Db 17093 ATTATGGGACGGAGGAGTACTTTTAAAAAATAAAAAA 17051

RESULT 9
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LOCUS Oryza sativa chromosome 3 BAC clone OSUNBb0069P02, complete
DEFINITION
AC145780
VERSION AC145780.2 GI:50872484
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 88044)
AUTHORS Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M.,
Overton II,L., Tsirlin,T., Kim,M., Bera,J., Jin,S., Fadrosch,D.W.,
Tallon,L., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.,
Riedmuller,S.B., Uterbach,T., Feldblyum,T., Yang,Q., Haas,B.,
Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and
Fraser,C.
TITLE Oryza sativa ssp. japonica cv. Nipponbare OSUNBb0069P02 BAC genomic
sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 88044)
AUTHORS Buell,R.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 88044)
AUTHORS Buell,R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jul 31, 2004 this sequence version replaced gi:33285037.
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ORIGIN
Query Match 5.6%; Score 99.2; DB 8; Length 88044;
Best Local Similarity 85.9%; Pred. No. 2.9e-13;
Matches 110; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Db 62909 ACTTTGGATATAAGTAAGTACAAGAAAAATAATAATTCRAATTTTAAATA 62968
Qy 61 AGACAGAGTGCTCAACAGTACAAGTAAACCTCAAAATTCCTTATATATGGGAC-TTATA 120
Db 62969 AGACAGAGTGCTTAACAGATGATAGCAAAATCTCAAAATTCCTTATATATGGGACGGAG 63028
Qy 121 TTATGGGA 128
Db 63029 AAGTAGGA 63036

FEATURES
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/notes="transposon02 TNP2-like transposon protein gi|4"
1532..2626
/gene="OSUNBb0067N01.1"
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RESULT 10
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LOCUS
DEFINITION
AC090485
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 159636)
AUTHORS de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K., King,L.,
Nascimento,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
Miller,B., Kuit,K., Cunnius,D.M., Rodriguez,S., Balija,V., Shah,R.,
Bahret,A., Yang,C., Bell,M., Palmer,L., O'Shaughnessy,A., Dedhia,N.
and McCombie,W.R.
TITLE Genomic Sequence for Oryza sativa, Nipponbare strain, clone
OSUNBa0067N01, from chromosome 3, complete sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159636)
AUTHORS McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA
REFERENCE 3 (bases 1 to 159636)
AUTHORS McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA
REFERENCE 4 (bases 1 to 159636)
AUTHORS Palmer,L.E., de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K.,
King,L., Nascimento,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
Miller,B., Kuit,K., Cunnius,D.M., Rodriguez,S., Balija,V., Shah,R.,
Bahret,A., Yang,C., Bell,M., O'Shaughnessy,A., Dedhia,N. and
McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY
11724, USA
REMARK
COMMENT
On Jun 20, 2001 this sequence version replaced gi:14209722.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest.
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PVFTALASQRLREVQAGDGLLRGLDAGRKARHRSVARLRALSVSFATAVAV
VAVGACIGVHLAAFAAPPMWGSFPAWGERFSGRAARRALVQLEAAKGTIYNLRDM
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SODSEADSEWNAQERQDGGFGRVGYREDPRGRSSTGRSSTYGSRYDTSQIE
IRPNSLDFRSGSVGRYDVGARHVDVITNGDKVYNSEPDQSGSASMLSQPQH
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LLPGVFPFPGGILLPGARGVDVNMVSNLPPPPVAGEHSTPGMGAGPNIHL
NOFGSIGAPTNGSLFHLQGTQSRMVGHPKPVGGWTPNRSNPTKAPSRGRQN
DYSQVDTGMGPONFIRELDLTSVAEDYPLKRLTQKDEIVAKSAPPMYKCDLR
QVLSPEPTEFDVILDPWEEYVAPGITDHTLEYNGEIEINLKTAEADTSP
VFLVQDGVGLSQGRQCLKNWFRRCEDVCWTKNKSATPSLRHDSHTILQSKBHC
LMGKGTVRSDVGHVHANIDTIIIDTGTGKPKEDMTRIIEHFALGRRLLEL
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PLEGLRPSKPPPHK"
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LFKIDFKVYINIKMSFYKMKAGFPDIDCDWTLKVKVGKGVAVRNVYQIGHYFTT
HKLQOGDPLSPLNIAADALTLIKRAEQGLIKGLGDMVRGVDILQADDTIC
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Evalue= e-174"
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Best Local Similarity 91.3%; Pred. No. 3.2e-13;
Matches 105; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1  ACTTTAGATAATAAGTACAGTACCAAGAAAAATAATAATAATTCAAAATTTTTTAAATA 60
Db      104069  ACTTTGATAATAAGTACAGTACCAAGAAAAATAATAATAATTCAAAATTTTTTAAATA 104010

QY      61  AGACGAGTGTGTCACACAGTACAGTAAAAAATCCCTATATATATATGAGAC 115
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RESULT 11

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[illegible]

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          pseudogene, ORF stop194 - rice tungro bacilliform virus"
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          25210..25330,25730..25775,26063..26140,26976..27082,
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          29091..29219))
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          25730..25775,26063..26140,26976..27082,28240..28300,
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          /gene="OJ1134_H03.5-2"
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28240..28300,28447..28506,28643..28725,28864..28974,
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Matches 106; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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QY 61 AGACGAGTGGTCAACAGTACAAAGTAAACAACTCAAAATTCCTTATATATGCGCTAT 119
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LOCUS
DEFINITION
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77 of the complete sequence.
ACCESSION
AE017105 AE016959
VERSION
AE017105.1 GI:31432655
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriartoideae; Oryzaceae; Oryza.
1 (bases 1 to 300029)
REFERENCE
AUTHORS
The Rice Chromosome 10 Sequencing Consortium
CONSTRM
In-depth view of structure, activity, and evolution of rice
TITLE
Chromosome 10
JOURNAL
Science 300, 1566-1569 (2003)
REFERENCE
2 (bases 1 to 300029)
AUTHORS
Buell,C.R., Wing,R.A., McCombie,W.R., Messing,J. and Yuan,Q.
TITLE
Direct Submission
JOURNAL
Submitted (05-MAY-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT
This is the pseudomolecule for rice chromosome 10, which was
constructed by resolving discrepancies between overlapping BACs,
trimming the overlap regions, and linking the unique sequences to
form a contiguous sequence. Genes in individual BAC clone were
identified by a combination of several methods: Gene prediction
programs, searches of the complete sequence against a peptide
database and EST databases. Genes with similarity to other proteins
are named after the database hits. Genes without significant
peptide similarity but with EST similarity are named as unknown
proteins. Genes without protein or EST similarity, that are
predicted by more than two gene prediction programs over most of
their length are annotated as hypothetical proteins. Genes
encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
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LOCUS AX656799 6669 from Patent WO03000898.
DEFINITION Sequence
ACCESSION AX656799

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VERSION AX656799.1 GI:29159613  
KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1  
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,  
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.  
TITLE Plant genes involved in defense against pathogens  
JOURNAL Patent: WO 03000898-A 6669 03-JAN-2003;  
Syngenta Participations AG (CH)  
FEATURES  
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QY 61 AGACGAGTGGTCAACAGTACAGTAAAAAATTCCTTATATTATGGGAC 115  
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Db 535 AGAGGAGTGGTCAACATTGTTAAGTAAAAAATCCAAATCCATTATATTATGGGAC 481  
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Search completed: November 17, 2004, 13:09:56  
Job time : 7355 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 09:30:30 ; Search time 824 Seconds  
(without alignments)

11288.804 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataaataagtaag.....ctcttccttcagtgcaag 1772

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_23Sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	1686	95.1	1686	4	Aaf24790 Nucleotid
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13	83	4.7	2000	10	Adc08414 Rice DNA
14	81.8	4.6	2000	8	Ada73166 Rice gene
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16	81.6	4.6	2000	8	Ada73455 Rice gene
17	81.6	4.6	2000	8	Ada71498 Rice gene
18	81	4.6	2000	8	Ada72521 Rice gene
19	80.4	4.5	2000	8	Ada72089 Rice gene
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27	79.6	4.5	2000	8	ADA71850	Ada71850 Rice gene
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42	70.2	4.0	2000	8	ADA72764	Ada72764 Rice gene
43	70.2	4.0	2000	8	ADA71501	Ada71501 Rice gene
44	69.4	3.9	1999	10	ADC08516	Adc08516 Rice DNA
45	69.2	3.9	2000	8	ADA71955	Ada71955 Rice gene

## ALIGNMENTS

RESULT 1  
AAP24785  
ID AAF24785 standard; DNA; 1772 BP.  
XX  
AC AAF24785;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a rice sucrose synthase 3 (RSus3) promoter.  
KW Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression;  
KW transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.  
OS Oryza sativa.  
PN WO200078975-A2.  
XX  
PD 28-DEC-2000.  
XX  
PF 15-JUN-2000; 2000WO-GB002641.  
XX  
PR 17-JUN-1999; 99GB-00014210.  
XX  
(DANI-) DANISCO AS.  
PI Donaldson IA, Rasmussen TB;  
XX  
DR WPI; 2001-071398/08.  
XX  
PT Rice sucrose synthase 3 promoter obtainable from plant genus Oryza,  
PT useful for expressing nucleotide sequence of interest in specific tissue  
or cell type e.g. endosperm.  
PS Claim 1; Page 142; 144pp; English.  
XX  
CC The present sequence represents a rice sucrose synthase 3 (RSus3)  
CC promoter. The RSus3 promoter has low homology with the RSus1 and RSus2  
CC promoters (7.7% and 4.6%, respectively). In addition, apart from  
CC conserved TATA box and intron splice sites, they have no motifs in  
CC common. The promoter can be used to prepare a product of interest,  
CC especially in the endosperm of a transgenic plant. Preferably, the  
CC promoter is used to cause expression of a nucleotide of interest that can  
CC affect carbohydrate metabolism, such as sucrose metabolism, in a plant  
CC tissue

XX	Sequence	1772 BP; 540 A; 368 C; 374 G; 490 T; 0 U; 0 Other;	
SQ	Query Match	100.0%; Score 1772; DB 4; Length 1772;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 1772; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ACTTTAGATAAATAAGTAAGTCAAGAGAAAATAAATAAATTTCCAAATTTTTTAATA	60
DB	1	ACTTTAGATAAATAAGTAAGTCAAGAGAAAATAAATAAATTTCCAAATTTTTTAATA	60
QY	61	AGACGAGTGTCAAAACAGTACAAAGTAAAACTCAAAATTCCTATATATATGGGACTTATA	120
DB	61	AGACGAGTGTCAAAACAGTACAAAGTAAAACTCAAAATTCCTATATATATGGGACTTATA	120
QY	121	TTATGGACGAGGAGAGTAGAAGATTGTAGCAAGAAAACAAAACAAAACACACCGC	180
DB	121	TTATGGACGAGGAGAGTAGAAGATTGTAGCAAGAAAACAAAACAAAACACACCGC	180
QY	181	CACCTGGCAGGCATGCACTTTAGTTCGGCAATTTGAGAGGTGCGCAGTAGACGATTACC	240
DB	181	CACCTGGCAGGCATGCACTTTAGTTCGGCAATTTGAGAGGTGCGCAGTAGACGATTACC	240
QY	241	CTACACAACTCTTCTTCAGTGAGTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300
DB	241	CTACACAACTCTTCTTCAGTGAGTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300
QY	301	CAGCAGCTAGCAACAGTTTTCAGGAAACAAATCGATAATCCATTGTCTCAGGAGGAAACATG	360
DB	301	CAGCAGCTAGCAACAGTTTTCAGGAAACAAATCGATAATCCATTGTCTCAGGAGGAAACATG	360
QY	361	GAGAAAAACCGGGCTGGAGACGAAACCGGAGACGTGTACCGTACGTTTCTGAAAGCTGA	420
DB	361	GAGAAAAACCGGGCTGGAGACGAAACCGGAGACGTGTACCGTACGTTTCTGAAAGCTGA	420
QY	421	ACCCATCTGCGAAATCCGAGATTTGTTGTTCAATCCCACTTGCAGTCTCTCAGATTG	480
DB	421	ACCCATCTGCGAAATCCGAGATTTGTTGTTCAATCCCACTTGCAGTCTCTCAGATTG	480
QY	481	GTTGATCTTCAACCGTATGATCATCTGAAAAATGAAGTGTAAATACCTTGAGAGACCT	540
DB	481	GTTGATCTTCAACCGTATGATCATCTGAAAAATGAAGTGTAAATACCTTGAGAGACCT	540
QY	541	TGATGGAAGCATGCTTCGAGGCGATTAGCTAAGAAAAAATAAATGTACTTTTCGAA	600
DB	541	TGATGGAAGCATGCTTCGAGGCGATTAGCTAAGAAAAAATAAATGTACTTTTCGAA	600
QY	601	ACTTAATTTTGGAGTAGATTAGGAGTGTTCCTATCGTAGTGATTTTCTACTATTGCA	660
DB	601	ACTTAATTTTGGAGTAGATTAGGAGTGTTCCTATCGTAGTGATTTTCTACTATTGCA	660
QY	661	GTTTAAACCGGCTAATAGTCAGATATAAAATTTTATCTATAGATCAATTTATAAATCATTTT	720
DB	661	GTTTAAACCGGCTAATAGTCAGATATAAAATTTTATCTATAGATCAATTTATAAATCATTTT	720
QY	721	TAGTTGCTTGGTTCATTTTCTACCACTTATCAACATAGCTCAACTGATCAATTTGACAA	780
DB	721	TAGTTGCTTGGTTCATTTTCTACCACTTATCAACATAGCTCAACTGATCAATTTGACAA	780
QY	781	TAAAGTTTACTAAACGACATCGCTCATACACACCCCAACCGCTCACCGATGGGTGCTCTC	840
DB	781	TAAAGTTTACTAAACGACATCGCTCATACACACCCCAACCGCTCACCGATGGGTGCTCTC	840
QY	841	GACACGAGTTTATGACATTTGTGCAACATATATCGGTGCGATGAAATCTACTGATGCGCC	900
DB	841	GACACGAGTTTATGACATTTGTGCAACATATATCGGTGCGATGAAATCTACTGATGCGCC	900
QY	901	ATGCGAAATTTAGCGTTCTGTTCAATGACGCTTCCACGGCACAGAGGCTGAGCAGAGCAT	960
DB	901	ATGCGAAATTTAGCGTTCTGTTCAATGACGCTTCCACGGCACAGAGGCTGAGCAGAGCAT	960
QY	961	GCATGATCGCTCTTCTGTAACAAAACAAAAGGTTTACTGGTAAATGACATGCTGCTGTAGCT	1020
DB	961	GCATGATCGCTCTTCTGTAACAAAACAAAAGGTTTACTGGTAAATGACATGCTGCTGTAGCT	1020

1021 AGTTAGCAGAAATGCAAGGCCCATGCAATGCTATGCAACAGTATAGTACCAAGCA 1080

1021 AGTTAGCAGAAATGCAAGGCCCATGCAATGCTATGCAACAGTATAGTACCAAGCA 1080

1081 TGATGTTAGTGGAGTAACTTAATCTATCAGCAGAGGAGCAAGCTCGTGCATGCTGTGAT 1140

1081 TGATGTTAGTGGAGTAACTTAATCTATCAGCAGAGGAGCAAGCTCGTGCATGCTGTGAT 1140

1141 GCATCTTCTCCAGTAACTTAGTGGTAAATTTTCCAAAAGCGTTGCTCATATGACAGT 1200

1141 GCATCTTCTCCAGTAACTTAGTGGTAAATTTTCCAAAAGCGTTGCTCATATGACAGT 1200

1201 AATTAGTAAATTTACCAAGGTTCAATCCGTTTACCTGACCAATACTACTCAGCAATG 1260

1201 AATTAGTAAATTTACCAAGGTTCAATCCGTTTACCTGACCAATACTACTCAGCAATG 1260

1261 GTATCTCTGGTTTTCGTTTAAACCGTTTGGTAAACCGTTTGGTAAACCGTTTGGTAAAC 1320

1261 GTATCTCTGGTTTTCGTTTAAACCGTTTGGTAAACCGTTTGGTAAACCGTTTGGTAAAC 1320

1321 AATTTTAAATTTAGTATTTTAACTTAGCAGGAGAAACCTTGAAGTTTGTGCTGTCG 1380

1321 AATTTTAAATTTAGTATTTTAACTTAGCAGGAGAAACCTTGAAGTTTGTGCTGTCG 1380

1381 AGCTGCTCTGGAGAGGAGGTTTGGTGGATTTGTAACCTGCTGTAACCTGCTGTAACCTGCT 1440

1381 AGCTGCTCTGGAGAGGAGGTTTGGTGGATTTGTAACCTGCTGTAACCTGCTGTAACCTGCT 1440

1441 TTTGAAACAGATATTTAGTGCACAAACAGCAAAATGCCAAACGATTTTTCGTTTACCGGCAA 1500

1441 TTTGAAACAGATATTTAGTGCACAAACAGCAAAATGCCAAACGATTTTTCGTTTACCGGCAA 1500

1501 GCTGAAGCTTTTACGATCCCATACCGCGTTGCTGCAAAACCTGCAAGAGAGAGCAGCA 1560

1501 GCTGAAGCTTTTACGATCCCATACCGCGTTGCTGCAAAACCTGCAAGAGAGAGCAGCA 1560

1561 GAAACAGGTGCTATTTTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620

1561 GAAACAGGTGCTATTTTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620

1621 GAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

1621 GAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

1681 TAAATACAGGTGGATGCAATCGCTCTCCAGCATCCATCGGTTCTCTGCTGCTGCTATCCA 1740

1681 TAAATACAGGTGGATGCAATCGCTCTCCAGCATCCATCGGTTCTCTGCTGCTGCTATCCA 1740

1741 TAGAGTTTCT 1772

1741 TAGAGTTTCT 1772

RESULT 2  
AAF24787  
ID AAF24787 standard; DNA; 1803 BP.  
XX  
AC AAF24787;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a rice sucrose synthase 3 (RSus3) promoter.  
XX  
KW Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression;  
transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.  
XX  
OS Oryza sativa.  
XX  
PN WO200078975-A2.  
XX  
PD 28-DEC-2000.



XX 15-JUN-2000; 2000WO-GB002641.  
 PF 17-JUN-1999; 99GB-00014210.  
 PR (DANI-) DANISCO AS.  
 XX Donaldson IA, Rasmussen TB;  
 XX WPI; 2001-071398/08.  
 XX Rice sucrose synthase 3 promoter obtainable from plant genus Oryza,  
 PT useful for expressing nucleotide sequence of interest in specific tissue  
 PT or cell type e.g. endosperm.  
 XX Disclosure; Page 143; 144pp; English.  
 PS  
 XX The present sequence represents a rice sucrose synthase 3 (RSus3)  
 CC promoter fragment. The RSus3 promoter has low homology with the RSus1 and  
 CC RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from  
 CC conserved TATA box and intron splice sites, they have no motifs in  
 CC common. The promoter can be used to prepare a product of interest,  
 CC especially in the endosperm of a transgenic plant. Preferably, the  
 CC promoter is used to cause expression of a nucleotide of interest that can  
 CC affect carbohydrate metabolism, such as sucrose metabolism, in a plant  
 CC tissue  
 XX  
 SQ Sequence 1803 BP; 551 A; 373 C; 383 G; 496 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1772; DB 4; Length 1803;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACTTTAGATAAATAAGTAGTACAAAGAAATAATAATAATTCAAATTTTTTAAATA 60  
 DB 1 ACTTTAGATAAATAAGTAGTACAAAGAAATAATAATAATTCAAATTTTTTAAATA 60  
 QY 61 AGACAGAGTGGTCAAAACAGTACAAAGTAAACAACTCAAAATTCCTTATATATGGACTTATA 120  
 DB 61 AGACAGAGTGGTCAAAACAGTACAAAGTAAACAACTCAAAATTCCTTATATATGGACTTATA 120  
 QY 121 TTATGGGACGGAGGAGTAGAAGATTGTAGCCAGAAAGAAACAAACAAACACACCGC 180  
 DB 121 TTATGGGACGGAGGAGTAGAAGATTGTAGCCAGAAAGAAACAAACAAACACACCGC 180  
 QY 181 CACCTGGCAGGAGTGCATCTTAGTGGCGCACATTTGAGAGGTGGCAGTAGACGAGTTACC 240  
 DB 181 CACCTGGCAGGAGTGCATCTTAGTGGCGCACATTTGAGAGGTGGCAGTAGACGAGTTACC 240  
 QY 241 CTACACAACTGCTTCTTCAGTCAGCTAGCTGCATGTTCTGTTCTGCATTTACATTGCAGG 300  
 DB 241 CTACACAACTGCTTCTTCAGTCAGCTAGCTGCATGTTCTGTTCTGCATTTACATTGCAGG 300  
 QY 301 CAGCAGCTAGCAACAGTTTGCAGGAAACATCCGATATCCATTGTGTCAGGAGGAAACATG 360  
 DB 301 CAGCAGCTAGCAACAGTTTGCAGGAAACATCCGATATCCATTGTGTCAGGAGGAAACATG 360  
 QY 361 GAGAAAAACCGGGGTGGAGACGAAACGGAGCAGCTGTACCGTTCGTAAGGCTGA 420  
 DB 361 GAGAAAAACCGGGGTGGAGACGAAACGGAGCAGCTGTACCGTTCGTAAGGCTGA 420  
 QY 421 ACCCATCTGCGAAATCCGAGATTCGTTTGTTCATTCGATTCGAGTCCTTCAGATTG 480  
 DB 421 ACCCATCTGCGAAATCCGAGATTCGTTTGTTCATTCGATTCGAGTCCTTCAGATTG 480  
 QY 481 GTTGATGTTCAACCGTAGTACATCTGAAAAATGAAGTGTAAATACCTTGAAGAGACT 540  
 DB 481 GTTGATGTTCAACCGTAGTACATCTGAAAAATGAAGTGTAAATACCTTGAAGAGACT 540  
 QY 541 TCATGGAAGCATGCTGCAGGCGATTAGCTAAGAAAAAATAAATGTAATTTTCGAA 600  
 DB 541 TCATGGAAGCATGCTGCAGGCGATTAGCTAAGAAAAAATAAATGTAATTTTCGAA 600

QY 601 ACTTAATTTTGGAGTTAGATTATTTAGGGTGTTCATCGTAGTGTATTTTCTACTATTGCA 660  
 DB 601 ACTTAATTTTGGAGTTAGATTATTTAGGGTGTTCATCGTAGTGTATTTTCTACTATTGCA 660  
 QY 661 GTTTAAACCGCTAATAGTCAGATATAAATTTTCTATATAGATCATTTATAAATCATTTT 720  
 DB 661 GTTTAAACCGCTAATAGTCAGATATAAATTTTCTATATAGATCATTTATAAATCATTTT 720  
 QY 721 TAGTTGCTTTCGTTTCATTTTCTACCACTTATCAACCATAGCTCAACTGATCAATTCGCAA 780  
 DB 721 TAGTTGCTTTCGTTTCATTTTCTACCACTTATCAACCATAGCTCAACTGATCAATTCGCAA 780  
 QY 781 TAAAGTTACTAAACGACATCGCTCATCAACACCAACGCTCACCGATGGGTGCTCTC 840  
 DB 781 TAAAGTTACTAAACGACATCGCTCATCAACACCAACGCTCACCGATGGGTGCTCTC 840  
 QY 841 GACCACGAGTTTAGCACTTGTGCAACATATATCGTGGCATGAACATCTACTATGCGCC 900  
 DB 841 GACCACGAGTTTAGCACTTGTGCAACATATATCGTGGCATGAACATCTACTATGCGCC 900  
 QY 901 ATGCGAATTTTAGCGTTTCGTTTCATGACGCTTCCAAACGACAGAGGCTGAGCAGCAGCAT 960  
 DB 901 ATGCGAATTTTAGCGTTTCGTTTCATGACGCTTCCAAACGACAGAGGCTGAGCAGCAGCAT 960  
 QY 961 GCATGATGCTCTTGTGTAACCAAAAAAGGTTACTGTGTAATGACATGCTGCTAGCT 1020  
 DB 961 GCATGATGCTCTTGTGTAACCAAAAAAGGTTACTGTGTAATGACATGCTGCTAGCT 1020  
 QY 1021 AGTTAGCAGATGCAAGGCCCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1080  
 DB 1021 AGTTAGCAGATGCAAGGCCCATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1080  
 QY 1081 TGTATGTTAGTACCACTAATCTATCAGCAGAGCAGCAGCTGCTGATGCTGATG 1140  
 DB 1081 TGTATGTTAGTACCACTAATCTATCAGCAGAGCAGCAGCTGCTGATGCTGATG 1140  
 QY 1141 GCATTTCTCAGTAACTCTAGTGGTAAATTTTCAACCAAGCGTGTCTCATATGACAGT 1200  
 DB 1141 GCATTTCTCAGTAACTCTAGTGGTAAATTTTCAACCAAGCGTGTCTCATATGACAGT 1200  
 QY 1201 AATTAGTAAATTTAGTAACTCTAGTGGTAAATTTTCAACCAAGCGTGTCTCATATGACAGT 1260  
 DB 1201 AATTAGTAAATTTAGTAACTCTAGTGGTAAATTTTCAACCAAGCGTGTCTCATATGACAGT 1260  
 QY 1261 GTATCTCTGTTTTCGTTTAAACCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1320  
 DB 1261 GTATCTCTGTTTTCGTTTAAACCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1320  
 QY 1321 AATTAAATTTAGTAACTCTAGTGGTAAATTTTCAACCAAGCGTGTCTCATATGACAGT 1380  
 DB 1321 AATTAAATTTAGTAACTCTAGTGGTAAATTTTCAACCAAGCGTGTCTCATATGACAGT 1380  
 QY 1381 AGCTGCTCTGGAAGAGCGTTTTCGTTTAAACCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1440  
 DB 1381 AGCTGCTCTGGAAGAGCGTTTTCGTTTAAACCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1440  
 QY 1441 TTTGAACAGATATTAGTGCACAGCAAAATGCAACCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1500  
 DB 1441 TTTGAACAGATATTAGTGCACAGCAAAATGCAACCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1500  
 QY 1501 GCTGAAGCTTTTACGATCCCATACCGCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1560  
 DB 1501 GCTGAAGCTTTTACGATCCCATACCGCGTGTGTAACCAAGCGTGTCTCATATGACAGT 1560  
 QY 1561 GAAACAGAGTTCATTTTGTGTTGGAAGCGCAAGTAAAGTAAACAGAGATGGAAGTAGT 1620  
 DB 1561 GAAACAGAGTTCATTTTGTGTTGGAAGCGCAAGTAAAGTAAACAGAGATGGAAGTAGT 1620  
 QY 1621 GAGGACAGGAGTGGAGCAGGAGCAGATGCGCCACCGCTCCCTGCAATTTTCGTTGTA 1680  
 DB 1621 GAGGACAGGAGTGGAGCAGGAGCAGATGCGCCACCGCTCCCTGCAATTTTCGTTGTA 1680  
 QY 1681 TAAATACAGGTGGATGCAATCGCTCTCCAGCATCCATCGTGTCTCTGCTGTTTCATCCA 1740





Db 901 ATCCGAATTTAGCGTTCTGTTCTGATGCGTTCCAAACGCGACAGAGGCTGAGCGACGAT 960  
 Qy 961 GCATGATGCTCTTGTGAAAAAAGGTTACTGTTAAATGACATGCTGCTGTAGCT 1020  
 Db 961 GCATGATGCTCTTGTGAAAAAAGGTTACTGTTAAATGACATGCTGCTGTAGCT 1020  
 Qy 1021 AGTTAGCAGATGCAAGCGCCATGATGATGCAATGCTATGCAACAGATATGATACGCA 1080  
 Db 1021 AGTTAGCAGATGCAAGCGCCATGATGATGCAATGCTATGCAACAGATATGATACGCA 1080  
 Qy 1081 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Db 1081 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
 Qy 1141 GCATCTCTCCAGTAACTAGTGTGTAATTTTACCCCAAGCGTTGCTCATATGACAGT 1200  
 Db 1141 GCATCTCTCCAGTAACTAGTGTGTAATTTTACCCCAAGCGTTGCTCATATGACAGT 1200  
 Qy 1201 AATTAGTAATATACCAAGGTTCAATCCCGTTACCTGACCAATATCTACTACGATG 1260  
 Db 1201 AATTAGTAATATACCAAGGTTCAATCCCGTTACCTGACCAATATCTACTACGATG 1260  
 Qy 1261 GTATCTCTGTTTGTGTAACCGTTGTAACCGTAACCGTAACCGTAACCGTAACCGTA 1320  
 Db 1261 GTATCTCTGTTTGTGTAACCGTTGTAACCGTAACCGTAACCGTAACCGTAACCGTA 1320  
 Qy 1321 AATTAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1380  
 Db 1321 AATTAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1380  
 Qy 1381 AGCTGCTCGGAGGAGCGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1440  
 Db 1381 AGCTGCTCGGAGGAGCGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1440  
 Qy 1441 TTTGACAGATATAGTGCACAGCAAAATGCAACGCAATTTTGTGTTTGTGTTTGTGTTTGT 1500  
 Db 1441 TTTGACAGATATAGTGCACAGCAAAATGCAACGCAATTTTGTGTTTGTGTTTGTGTTTGT 1500  
 Qy 1501 GCTGAAGCTTTTACGATCCCATACCGCGTTGCTGCAAACTGCAAGAGAGAGAGAGAG 1560  
 Db 1501 GCTGAAGCTTTTACGATCCCATACCGCGTTGCTGCAAACTGCAAGAGAGAGAGAGAG 1560  
 Qy 1561 GAAACAGGTGCTATTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1620  
 Db 1561 GAAACAGGTGCTATTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1620  
 Qy 1621 GAGGACCGGAGTGCAGGAGGAGACATGCGCGCTCCCTGCAATTTTGTGTTGTTGTTGTT 1680  
 Db 1621 GAGGACCGGAGTGCAGGAGGAGACATGCGCGCTCCCTGCAATTTTGTGTTGTTGTTGTT 1680  
 Qy 1681 TAAATA 1686  
 Db 1681 TAAATA 1686

RESULT 5  
 ADA73179  
 ID ADA73179 standard; DNA; 2000 BP.  
 XX  
 AC ADA73179;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Rice gene, SEQ ID 6505.  
 XX  
 DE Plant; bacterial infection; fungal infection; viral infection; rice;  
 KW gene; ds.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO2003000898-A1.  
 XX

PD 03-JAN-2003.  
 XX 22-JUN-2001; 2001WO-IB001105.  
 XX 22-JUN-2001; 2001WO-IB001105.  
 PR (SYGN) SYNGENTA PARTICIPATIONS AG.  
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,  
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
 XX WPI; 2003-175290/17.  
 DR Identifying at least one gene involved in plant resistance or response to  
 XX pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 XX gene expression.  
 PS Claim 27; SEQ ID NO 6505; 899pp; English.  
 XX The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.  
 XX  
 SQ Sequence 2000 BP; 520 A; 394 C; 427 G; 658 T; 0 U; 1 Other;

Query Match 61.1%; Score 1082.4; DB 8; Length 2000;  
 Best Local Similarity 99.3%; Pred. No. 3.2e-279;  
 Matches 1098; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
 Qy 669 CGCTAATAGTCAGATATAAAATTTTATCTATAGATCAATTTATAATCAATTTTATGTTCT 728  
 Db 1 CGCTAATAGTCAGATATAAAATTTTATCTATAGATCAATTTATAATCAATTTTATGTTCT 60  
 Qy 729 TCGTTCAATTTTCAACCTTATCAACATAGCTCACTCAATTTGATCAATTTGATTTGCT 788  
 Db 61 TCGTTCAATTTTCAACCTTATCAACATAGCTCACTCAATTTGATCAATTTGATTTGCT 120  
 Qy 789 ACTAAACGACATCGCTCATCACACACCAACCGCTCACCGATGGTGGCTCTCGACACCA 848  
 Db 121 ACTAAACGACATCGCTCATCACACACCAACCGCTCACCGATGGTGGCTCTCGACACCA 180  
 Qy 849 GTTTAGCACTTGTGCAACATATATGCTGCGATGAACATCTACTGATGCGCATGCAAT 908  
 Db 181 GTTTAGCACTTGTGCAACATATATGCTGCGATGAACATCTACTGATGCGCATGCAAT 240  
 Qy 909 TTTAGGTTGTTTCAATGAGCTTCCAAACGCGACAGAGGCTGAGCAGCATGCAAT 968  
 Db 241 TTTAGGTTGTTTCAATGAGCTTCCAAACGCGACAGAGGCTGAGCAGCATGCAAT 300  
 Qy 969 GGCTCTTGTGAAAAAAGGTTACTGTTAAATGACATGCTGCTGTAGTTAGTGA 1028  
 Db 301 GGCTCTTGTGAAAAAAGGTTACTGTTAAATGACATGCTGCTGTAGTTAGTGA 360  
 Qy 1029 GAATGCAAGCGCCATGCAATGCAATGCTATGCAACAGATATAGTACGAGCATGTTGCT 1088  
 Db 361 GAATGCAAGCGCCATGCAATGCAATGCTATGCAACAGATATAGTACGAGCATGTTGCT 420  
 Qy 1089 AGCAGCTAACTAACTATCAGCAGAGGAGCAAGCTCGTGCATGCTGTGATGCTACTTCT 1148  
 Db 421 AGCAGCTAACTAACTATCAGCAGAGGAGCAAGCTCGTGCATGCTGTGATGCTACTTCT 480  
 Qy 1149 CTCAGTAACTAGTGGTAAATTTTACCCCAAGCGTTGCTCATATGACAGTAAATAGTA 1208  
 Db 481 CTCAGTAACTAGTGGTAAATTTTACCCCAAGCGTTGCTCATATGACAGTAAATAGTA 540







DR WPI; 2002-372312/40.  
 XX P-PSDB; AAO17798.  
 PT Rice-originated gene, Spi7, that inhibits lesion formation and is  
 PT applicable in improving heat stress of plants thus leading to prevention  
 PT of lesion formation, for developing new breeds of plants for agriculture  
 PT and horticulture.  
 XX Claim 1; Page 30-40; 53pp; Japanese.  
 XX  
 CC The present invention provides the protein and coding sequences of rice  
 CC lesion formation inhibitor Spi7. The protein improves the heat stress of  
 CC the plant, and can be used in the development of new breeds of plants for  
 CC agriculture and horticulture. The present sequence is the coding sequence  
 CC of the invention  
 XX  
 SQ Sequence 5579 BP; 1453 A; 1272 C; 1235 G; 1619 T; 0 U; 0 Other;  
 Query Match 4.8%; Score 85.8; DB 6; Length 5579;  
 Best Local Similarity 88.2%; Pred. No. 6.2e-12;  
 Matches 105; Conservative 0; Mismatches 12; Indels 2; Gaps 1;  
 QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAATAATAATTCCTTATATATGGGACTTAT 60  
 DB 2257 ACTTTAGATAATAAGTAAGT--CAAAAAGAGATAATAATAATTTTAAATTTTAAATA 2314  
 QY 61 AGACGAGTGTGTCACAGTACAGTAACTCAAAATTCCTTATATATGGGACTTAT 119  
 DB 2315 AGACGATGTCACAGTCAAGTCAATAATAAACTCAAGATCCCTTATATATGGGATAAT 2373  
 RESULT 10  
 ADA72806/c  
 ID ADA72806 standard; DNA; 2000 BP.  
 XX  
 AC ADA72806;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Rice gene, SEQ ID 6131.  
 XX  
 KW Plant; bacterial infection; fungal infection; viral infection; rice;  
 KW gene; ds.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO2003000898-A1.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 22-JUN-2001; 2001WO-IB001105.  
 XX  
 PR 22-JUN-2001; 2001WO-IB001105.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
 XX WPI; 2003-175290/17.  
 XX  
 PT Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.  
 XX  
 XX Claim 27; SEQ ID NO 6131; 899pp; English.  
 XX  
 CC The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.  
 XX

SQ Sequence 2000 BP; 575 A; 481 C; 470 G; 467 T; 0 U; 7 Other;

Query Match 4.8%; Score 85.4; DB 8; Length 2000;  
 Best Local Similarity 89.6%; Pred. No. 4.9e-12;  
 Matches 103; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAATAATAATTCCTTATATATGGGACTTAT 60  
 DB 624 ACTTTGAATAATAAGTAAGTCACAGATAATAATAATAATTTTAAATTTTAAATA 566  
 QY 61 AGACGAGTGTGTCACAGTACAGTAACTCAAAATTCCTTATATATGGGACTTAT 115  
 DB 565 AGACGAATAGTCAACAGTCAAGTCAAAATTCCTTATATATGGGACTTAT 511

RESULT 11

ADJ41087/c  
 ID ADJ41087 standard; cDNA; 2000 BP.

XX

AC ADJ41087;

XX

DT 06-MAY-2004 (first entry)

XX

DE Plant cDNA #2087.

XX

KW Plant; gene; ss; transcription; plant genome augmentation; cereal;

KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;

KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;

KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;

KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;

KW antifungal.

XX

OS Eukaryota.

XX

PN US2004016025-A1.

XX

PD 22-JAN-2004.

XX

PF 26-SEP-2002; 2002US-00260238.

XX

PR 26-SEP-2001; 2001US-0325277P.

XX

PR 26-SEP-2001; 2001US-0325448P.

XX

PR 04-APR-2002; 2002US-0370620P.

XX

(BUDW/) BUDWORTH P.

PA (MOUG/) MOUGHAMER T.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

PA (ZHUT/) ZHU T.

XX

XX

PI Budworth P, Moughamer T, Briggs SP, Provart N, Ricke D, Zhu T;

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	Query Match	4.7%	Score 83.2	DB 12	Length 900
	Best Local Similarity	87.9%	Fred. No. 1.3e-11		
	Matches 102	Conservative 0	Mismatches 13	Indels 1	Gaps 1
QY	1	ACTTTAGATAATAAGTAAAGTCACAGAAAAATAAATAATAATTC-AAAATTTTTTAAAT	59		
DB	119	ACTCTGGATATATAAGTAAAGTCACAAATAAATAATAATAATTTCAAATTTTCTGAAT	178		
QY	60	AAGACGAGTGGTCAAAACAGTACAGTAAAAAATCTCAAAATTCCTTATATTATGGGAC	115		
DB	179	AAGACGAATGGTCAAAACAGTGCAGTAAATGTCAAAATCCCTTATATTATTAAGGGAC	234		



XX Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.  
XX Oryza sativa.  
XX WO2003000898-A1.  
XX 03-JAN-2003.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri P, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.  
XX Claim 27; SEQ ID NO 4820; 899pp; English.  
XX The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to that expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.  
XX SQ Sequence 2000 BP; 713 A; 326 C; 345 G; 616 T; 0 U; 0 Other;  
Query Match 4.6%; Score 81.6; DB 8; Length 2000;  
Best Local Similarity 87.1%; Pred. No. 5.1e-11;  
Matches 101; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
QY 1 ACTTTAGATAATAAGTAAGTCACAGAAATAATAATAATCC-AAATTTTTTAAT 59  
423 ACTGTGGATAATAAGTAAGTCACAAATGAAATAATAATAATTTCAAAATTTTGAAT 482  
Db  
QY 60 AAGACGAGTGGTCAACAGTACAACTCAAAATCCTTATATATATCGGAC 115  
Db 483 AAGACGAGTGGTCAACAGTACAACTCAAAATCCTTATATATATGAGAC 538  
Search completed: November 17, 2004, 11:07:15  
Job time : 830 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 10:46:50 ; Search time 174 Seconds  
(without alignments)  
7238.609 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 acttagataataagaag.....ctctctctcttcagtgcag 1772

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
C 1	47.2	2.7	7218	1	US-08-232-463-14
C 2	45.6	2.6	640881	4	Sequence 14, Appl
C 3	43	2.4	832	4	Sequence 1, Appl
4	42.8	2.4	1141	4	Sequence 2813, Ap
5	42	2.4	3602	4	Sequence 22, Appl
6	40.2	2.3	640681	4	Sequence 1, Appl
7	39	2.2	3738	4	Sequence 1, Appl
8	39	2.2	3926	4	Sequence 3978, Ap
9	38.6	2.2	8607	4	Sequence 4015, Ap
10	38.4	2.2	450	4	Sequence 71, Appl
11	38.4	2.2	81001	4	Sequence 12394, A
12	38.2	2.2	195	4	Sequence 1, Appl
13	38.2	2.2	1141	4	Sequence 8025, Ap
14	38.2	2.2	195	4	Sequence 23307, A
15	38	2.1	1242	4	Sequence 22, Appl
16	37.8	2.1	3758	3	Sequence 352, App
17	37.8	2.1	4383	3	Sequence 1, Appl
18	37.8	2.1	4383	3	Sequence 2, Appl
19	37.8	2.1	5175095-4	6	Patent No.5175095
20	37.8	2.1	517307-1	6	Patent No. 517307
C 21	37.6	2.1	6070	4	US-10-204-708-10
C 22	37.6	2.1	1017	4	Sequence 10, Appl
23	37.6	2.1	1092	3	Sequence 1003, Ap
24	37.6	2.1	2071	3	US-09-134-001C-1876
25	37.6	2.1	2781	3	Sequence 1876, Ap
26	37.6	2.1	3285	4	Sequence 5, Appl
27	37.4	2.1	3126	4	Sequence 4, Appl
					Sequence 4141, Ap
					Sequence 28, Appl
					Sequence 3912, Ap

28	37.4	2.1	5735	4	US-09-734-674-1	Sequence 1, Appl
29	37.4	2.1	11015	4	US-10-204-708-55	Sequence 55, Appl
C 30	37.4	2.1	202001	4	US-09-734-674-3	Sequence 3, Appl
31	37.4	2.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl
32	37.4	2.1	1664976	4	US-09-692-570-1	Sequence 3, Appl
33	37	2.1	786431	4	US-09-751-389-3	Sequence 1, Appl
C 34	36.8	2.1	505	4	US-09-621-976-15639	Sequence 15639, A
35	36.8	2.1	691	4	US-09-270-767-29557	Sequence 29557, A
36	36.8	2.1	1356	4	US-09-270-767-13559	Sequence 13559, A
37	36.8	2.1	5392	4	US-08-880-006-5	Sequence 5, Appl
38	36.4	2.1	359	4	US-03-270-767-3877	Sequence 3877, Ap
39	36.4	2.1	359	4	US-09-270-767-19159	Sequence 19159, A
40	36.4	2.1	365	4	US-09-621-976-16042	Sequence 16042, A
41	36.4	2.1	371	4	US-09-621-976-16048	Sequence 16048, A
C 42	36.4	2.1	881	4	US-08-956-171E-518	Sequence 518, App
C 43	36.4	2.1	881	4	US-08-781-986A-518	Sequence 518, App
C 44	36.4	2.1	1055	4	US-09-806-708B-23	Sequence 23, Appl
C 45	36.4	2.1	6317	4	US-10-204-708-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-Fls  
; US-08-232-463-14

Query Match

2.7%; Score 47.2; DB 1; Length 7218;





Db 125580 ATAAATGTTTTTATGGTTTATGGCTTAATATGCTTTTATCAATCAATAAACAATA 125639  
Qy 760 GCTCAACTGATCAATGACATAAAAGTTACTAAACG 796  
Db 125640 AATATTTTCAATTAATTAATCAATGTTCTTCACG 125676

RESULT 7  
US-09-710-279-3978  
; Sequence 3978, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3978  
; LENGTH: 3738  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-3978

Query Match 2.2%; Score 39; DB 4; Length 3738;  
Best Local Similarity 52.1%; Pred. No. 0.9;  
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
Qy 559 AGCGATTAGCTAAGAAAAAAATAAATGTAATCTTTTCGAACTTAATTTGGAGTTAG 618  
Db 111 AAGTATCATCAATGTAATCAATATCTCTTTTATAAATGATTTTGGCTTAACA 170  
Qy 619 ATTTTAGGGTGTTCATCGTAGTATTTCTACTATTCGAGTTTAAACCGCTTAATAGT 678  
Db 171 ATCATAGTTACTAAATCTGTGCTTACTCTTTTCAATGAATCAATCACTCTATAGAT 230  
Qy 679 CAGATATAAATTTATCTATAGATCAATTTAATATCAATTTTAGTT 725  
Db 231 AACTAATTTATTTAATTTAATAAATTAATTTCTTTTATTAAT 277

RESULT 8  
US-09-710-279-4015  
; Sequence 4015, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: P03480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4015  
; LENGTH: 3926  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-4015  
Query Match 2.2%; Score 39; DB 4; Length 3926;  
Best Local Similarity 52.1%; Pred. No. 0.92;

Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
Qy 559 AGCGATTAGCTAAGAAAAAAATAAATGTAATCTTTTCGAACTTAATTTGGAGTTAG 618  
Db 3505 AAGTATCATCAATGTAATCAATATCTCTTTTATAAATGATTTTGGCTTAACA 3564  
Qy 619 ATTTTAGGGTGTTCATCGTAGTATTTCTACTATTCGAGTTTAAACCGCTTAATAGT 678  
Db 3565 ATCATAGTTACTAAATCTGTGCTTACTCTTTTTCATGAATGATCACTCTCTATAGAT 3624  
Qy 679 CAGATATAAATTTATCTATAGATCAATTTAATAATCAATTTTAGTT 725  
Db 3625 AACTAATTTATTTAATTTAATAAATTAATTTCTTTTATTAAT 3671

RESULT 9  
US-10-204-708-71  
; Sequence 71, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 71  
; LENGTH: 8607  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-71

Query Match 2.2%; Score 38.8; DB 4; Length 8607;  
Best Local Similarity 51.8%; Pred. No. 1.6;  
Matches 88; Conservative 0; Mismatches 82; Indels 0; Gaps 0;  
Qy 574 AAAAAAATAAATGTAATCTTTTCGAACTTAATTTGGAGTTAGTTTAGGGTGTTC 633  
Db 7620 AAAAGATATTTTACGCTGCTGATGATTTTATAATTTATTTGAAATTTGAGTTGTAT 7679  
Qy 634 CATCTAGTATTTTCTACTATTCAGTTTAAACCGCTTAATAGTCAGATATAAATTT 693  
Db 7680 TAAATTTAGTTTATTTTATTTGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTT 7739  
Qy 694 ATCTATAGATCAATTTAATAATCAATTTTAGTTGCTTCGTTCAATTTTCTA 743  
Db 7740 TTATATGATTTTATTTTATAGTTATCTTTTATTTTATTTTATTTTATTTTATTTT 7789  
RESULT 10  
US-09-270-767-12394  
; Sequence 12394, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7328-094  
; CURRENT APPLICATION NUMBER: US/09/270,767



```
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12394
/ LENGTH: 450
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
US-09-270-767-12394

Query Match      2.2%; Score 38.6; DB 4; Length 450;
Best Local Similarity 51.4%; Pred. No. 0.37;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 6 AGATATAAGTAAGTCACAGAAATATAATTAATTCCTTATATATGGACTTATATTG 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AGCATGTCAGAAACCAAGATAATATATATATATATATATATATATATATATAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 66 AGTGGTCAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TAATGTAAATCAACACACACATTCCTTATTAATTAATTAATTAATTAATTA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 126 GGACGAGGAAGTAGAAGATTGTAGCAAGAAACCAACCAACCAACCAACCAAC 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ATAAATATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAACC 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-09-750-580-1/c
/ Sequence 1, Application US/09750580
/ Patent No. 6455280
/ GENERAL INFORMATION:
/ APPLICANT: Yen, Frances
/ APPLICANT: Denison, Blake
/ APPLICANT: Bour, Barbara
/ APPLICANT: Bihain, Bernard
/ APPLICANT: Dumas Milne Edwards, Jean-Baptiste
/ APPLICANT: Duclert, Aymeric
/ APPLICANT: Bougueleret, Lydie
/ APPLICANT: Ebbets-Reed, Dana
/ APPLICANT: Salter-Cid, Luisa
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
/ FILE REFERENCE: 89, US2.CIP
/ CURRENT APPLICATION NUMBER: US/09/750,580
/ CURRENT FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: US 09/599,362
/ PRIOR FILING DATE: 2000-06-21
/ PRIOR APPLICATION NUMBER: PCT/IB00/0101
/ PRIOR FILING DATE: 2000-06-21
/ PRIOR APPLICATION NUMBER: PCT/IB99/02058
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: US 49/469/099
/ PRIOR FILING DATE: 1999-12-21
/ PRIOR APPLICATION NUMBER: US 60/113,686
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: US 60/141,032
/ PRIOR FILING DATE: 1999-06-25
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1
/ LENGTH: 81001
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: 10946..12946
/ OTHER INFORMATION: 5'regulatory region
/ NAME/KEY: exon
/ LOCATION: 12947..12958
/ OTHER INFORMATION: exon 1
/ NAME/KEY: exon
/ LOCATION: 13470..13526
/ OTHER INFORMATION: exon 2
/ NAME/KEY: exon
/ LOCATION: 12348..12366
```

```
/ LOCATION: 13641..13752
/ OTHER INFORMATION: exon 3
/ NAME/KEY: exon
/ LOCATION: 14271..15968
/ OTHER INFORMATION: exon 4
/ NAME/KEY: misc.feature
/ LOCATION: 15969..17969
/ OTHER INFORMATION: 3'regulatory region
/ NAME/KEY: allele
/ LOCATION: 1239
/ OTHER INFORMATION: 20-828-311 : polymorphic base C or T
/ NAME/KEY: allele
/ LOCATION: 12347
/ OTHER INFORMATION: 17-42-319 : polymorphic base C or T
/ NAME/KEY: allele
/ LOCATION: 15241
/ OTHER INFORMATION: 17-41-250 : polymorphic base C or T
/ NAME/KEY: allele
/ LOCATION: 42218
/ OTHER INFORMATION: 20-841-149 : polymorphic base A or G
/ NAME/KEY: allele
/ LOCATION: 45442
/ OTHER INFORMATION: 20-842-115 : polymorphic base A or G
/ NAME/KEY: allele
/ LOCATION: 77058
/ OTHER INFORMATION: 20-853-415 : polymorphic base C or T
/ NAME/KEY: primer bind
/ LOCATION: 929..949
/ OTHER INFORMATION: 20-828.pu
/ NAME/KEY: primer bind
/ LOCATION: 1357..1377
/ OTHER INFORMATION: 20-828.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 12029..12050
/ OTHER INFORMATION: 17-42.pu
/ NAME/KEY: primer bind
/ LOCATION: 12581..12603
/ OTHER INFORMATION: 17-42.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 14992..15012
/ OTHER INFORMATION: 17-41.pu
/ NAME/KEY: primer bind
/ LOCATION: 15460..15482
/ OTHER INFORMATION: 17-41.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 42070..42090
/ OTHER INFORMATION: 20-841.pu
/ NAME/KEY: primer bind
/ LOCATION: 42572..42591
/ OTHER INFORMATION: 20-841.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 45328..45347
/ OTHER INFORMATION: 20-842.pu
/ NAME/KEY: primer bind
/ LOCATION: 45863..45883
/ OTHER INFORMATION: 20-842.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 76644..76664
/ OTHER INFORMATION: 20-853.pu
/ NAME/KEY: primer bind
/ LOCATION: 77166..77185
/ OTHER INFORMATION: 20-853.rp complement
/ NAME/KEY: primer bind
/ LOCATION: 1220..1238
/ OTHER INFORMATION: 20-828-311.mis
/ NAME/KEY: primer bind
/ LOCATION: 1240..1258
/ OTHER INFORMATION: 20-828-311.mis complement
/ NAME/KEY: primer bind
/ LOCATION: 12328..12346
/ OTHER INFORMATION: 17-42-319.mis
/ NAME/KEY: primer bind
/ LOCATION: 12348..12366
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OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42205..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match      2.2%; Score 38.4; DB 4; Length 81001;
Best Local Similarity 50.5%; Pred. No. 7.2;
Matches 93; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 10 AATAAGTAGTCACAGAGAAATAATAATTCCTTATATATGGGACTTATATATGGAG 69
Db 52930 AAGCAGGGTGACAAAGGGAATAAGAGAGAAATCTAGGATAAATCAGAACAGAGT 52871

Qy 70 GTCAACAGTACAGTAAATACTCAAAATTCCTTATATATGGGACTTATATATGGGAC 129
Db 52870 GGAATAAGCACTGAGAGAAATAGACAAATTAATAGTAAATAAATCTAGTCA 52811

Qy 130 GGAGGAGTAGAGAGTGTAGCCAGAGAAAAACAAACACACACCGCCACTGGCA 189
Db 52810 GGGAGAGTCTCTAGTTTGGGTCCCAAAATTTAAAAACAAAAAATCTCGGTAGCA 52751

Qy 190 GGCA 193
Db 52750 GGGA 52747

RESULT 12
US-09-767-8025
; Sequence 8025, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

```

```

FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8025
LENGTH: 195
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-8025

Query Match      2.2%; Score 38.2; DB 4; Length 195;
Best Local Similarity 52.1%; Pred. No. 0.31;
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 7 GATAATAAGTAGTCACAGAGAAAAATAATAATAATTCCTTATATATGGGACTTATATGG 126
Db 33 GATCAGTAAACACATCACAAAAAAGAACTCAGTCTCACATAATTTGGGGCTCAACA 92

Qy 67 GTGTCACACAGTACAGTAAATACTCAAAATTCCTTATATATGGGACTTATATGG 126
Db 93 ATTAATATACACAAATTAACCAAAATACAGAGTGTAAAGGTAGTAACAGTGTGA 152

Qy 127 GACGGAGGAGTAGAGATTGTAGCCAGAGAAAAACAAAAAC 169
Db 153 AAAACAGAAATTAATAATATATGAAAAAAGAAAAAAGAAAAAC 195

RESULT 13
US-09-270-767-23307
; Sequence 23307, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23307
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23307

Query Match      2.2%; Score 38.2; DB 4; Length 195;
Best Local Similarity 52.1%; Pred. No. 0.31;
Matches 85; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 7 GATAATAAGTAGTCACAGAGAAAAATAATAATAATTCCTTATATATGGGACTTATATGG 126
Db 33 GATCAGTAAACACATCACAAAAAAGAACTCAGTCTCACATAATTTGGGGCTCAACA 92

Qy 67 GTGTCACACAGTACAGTAAATACTCAAAATTCCTTATATATGGGACTTATATGG 126
Db 93 ATTAATATACACAAATTAACCAAAATACAGAGTGTAAAGGTAGTAACAGTGTGA 152

Qy 127 GACGGAGGAGTAGAGATTGTAGCCAGAGAAAAACAAAAAC 169
Db 153 AAAACAGAAATTAATAATATATGAAAAAAGAAAAAAGAAAAAC 195

RESULT 14
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 13:10:01 ; Search time 901 Seconds  
(without alignments)  
10627.326 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
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- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 1	134.4	7.6	187	17	US-10-437-963-100861
C 2	87.8	5.0	2000	16	US-10-260-238-1841
C 3	85.8	4.8	5579	16	US-10-168-273B-1
C 4	84.2	4.8	2000	16	US-10-260-238-2087
C 5	80.4	4.5	12120	10	US-09-840-743-19
C 6	80.4	4.5	2000	16	US-10-260-238-2150
C 7	78.4	4.4	2000	16	US-10-260-238-2454
C 8	76.8	4.3	1912	16	US-10-260-238-1722
C 9	76.8	4.3	2000	16	US-10-260-238-1664
C 10	75.4	4.2	6064	17	US-10-437-963-10006
C 11	73.8	4.2	2000	16	US-10-260-238-2176
C 12	73.4	4.1	5216	17	US-10-437-963-50400

C 13	72.8	4.1	2000	16	US-10-260-238-1731
C 14	72.2	4.1	2955	17	US-10-437-963-34025
C 15	69	3.9	1480	17	US-10-437-963-43365
C 16	69	3.9	2000	16	US-10-260-238-2535
C 17	68.2	3.8	1256	17	US-10-437-963-36881
C 18	67	3.8	576	17	US-10-437-963-37198
C 19	65.6	3.7	2000	16	US-10-260-238-2448
C 20	63	3.6	981	17	US-10-437-963-59741
C 21	63	3.6	2000	16	US-10-260-238-2163
C 22	62.4	3.5	633	17	US-10-437-963-49505
C 23	62.2	3.5	712	17	US-10-437-963-92669
C 24	62.2	3.5	2000	16	US-10-260-238-1963
C 25	62	3.5	2413	17	US-10-437-963-64377
C 26	62	3.5	5579	16	US-10-168-273B-1
C 27	62	3.5	6064	17	US-10-437-963-10006
C 28	61.4	3.5	1476	17	US-10-437-963-40280
C 29	61	3.4	359	17	US-10-437-963-87728
C 30	60.6	3.4	2000	16	US-10-260-238-1949
C 31	60.4	3.4	2000	16	US-10-260-238-2535
C 32	59.6	3.4	630	17	US-10-437-963-27816
C 33	59.4	3.4	2000	16	US-10-260-238-2655
C 34	58.6	3.3	1373	17	US-10-437-963-97110
C 35	58	3.3	680	17	US-10-437-963-53353
C 36	57.2	3.2	433	17	US-10-437-963-4401
C 37	56.8	3.2	2981	17	US-10-437-963-92628
C 38	56	3.2	2000	16	US-10-260-238-1727
C 39	55.6	3.1	548	17	US-10-437-963-45047
C 40	55.6	3.1	1256	17	US-10-437-963-36681
C 41	53.2	3.0	2000	16	US-10-260-238-1731
C 42	52.4	3.0	2000	16	US-10-260-238-2225
C 43	51.6	2.9	433	17	US-10-437-963-4401
C 44	51.4	2.9	1480	17	US-10-437-963-43365
C 45	51.4	2.9	2000	16	US-10-260-238-2448

## ALIGNMENTS

RESULT 1  
US-10-437-963-100861/c  
; Sequence 100861, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 100861  
; LENGTH: 187  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_98536C.1  
US-10-437-963-100861

Query Match 7.6%; Score 134.4; DB 17; Length 187;  
Best Local Similarity 85.6%; Pred. No. 1.1e+23;  
Matches 161; Conservative 0; Mismatches 26; Indels 1; Gaps 1;  
QY 190 GGCATGCATCTTAGTTCGGCAGCATTCAGAGGTTCGAGTAGCAGGTACCTACACAC 249  
DB 187 GGCATGCATCTTAGTTCGGCAGCATTCAGAGGTTCGAGTAGCAGGTACCTACACAC 128

Sequence 1731, Ap  
Sequence 34025, A  
Sequence 43365, A  
Sequence 2535, Ap  
Sequence 36881, A  
Sequence 37198, A  
Sequence 2448, Ap  
Sequence 59741, A  
Sequence 2163, Ap  
Sequence 49505, A  
Sequence 92669, A  
Sequence 1963, Ap  
Sequence 64377, A  
Sequence 1, Appli  
Sequence 10006, A  
Sequence 40280, A  
Sequence 87728, A  
Sequence 1949, Ap  
Sequence 2535, Ap  
Sequence 27816, A  
Sequence 2655, Ap  
Sequence 97110, A  
Sequence 53353, A  
Sequence 4401, Ap  
Sequence 92628, A  
Sequence 1727, Ap  
Sequence 45047, A  
Sequence 36681, A  
Sequence 1731, Ap  
Sequence 2225, Ap  
Sequence 4401, Ap  
Sequence 43365, A  
Sequence 2448, Ap



FEATURE:  
 NAME/KEY: N region  
 LOCATION: (433)..(433)  
 OTHER INFORMATION: n = any nucleotide  
 FEATURE:  
 NAME/KEY: N region  
 LOCATION: (1346)..(1346)  
 OTHER INFORMATION: n = any nucleotide  
 FEATURE:  
 NAME/KEY: N region  
 LOCATION: (1355)..(1355)  
 OTHER INFORMATION: n = any nucleotide  
 FEATURE:  
 NAME/KEY: N region  
 LOCATION: (1386)..(1386)  
 OTHER INFORMATION: n = any nucleotide  
 FEATURE:  
 NAME/KEY: N region  
 LOCATION: (1394)..(1394)  
 OTHER INFORMATION: n = any nucleotide  
 FEATURE:  
 NAME/KEY: N region  
 LOCATION: (1402)..(1402)  
 OTHER INFORMATION: n = any nucleotide  
 US-10-260-238-2087

Query Match 4.8%; Score 84.2; DB 16; Length 2000;  
 Best Local Similarity 88.0%; Pred. No. 2e-10;  
 Matches 103; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
 QY 3 TTTAGATAATAAGTAAGTACCAAGAAAATAATAATTCACAAATTTTTTTTAATAAG 62  
 DB 344 TTGGATAATAAGTAAGTACCAAGAAAATAATAATTCACAAATTTTTTTTAATAAG 286  
 QY 63 ACAGTGGTCAACAGTACAGTAAACCTCAAAATTCCTTATATTATGGGACTTAT 119  
 DB 285 ATGAGTGGTCAACAGTGGTCAAGCAAACTCAAAATCCCTTATATTATGGGACGGAT 229

RESULT 5  
 US-09-840-743-19/c  
 Sequence 19, Application US/09840743  
 Publication No. US20030135890A1  
 GENERAL INFORMATION:  
 APPLICANT: Fischer, Robert L.  
 APPLICANT: Choi, Yoonhee  
 APPLICANT: Hannon, Mike  
 APPLICANT: Okumuro, Jack Kishiro  
 APPLICANT: Tatarinova, Tatiana Valerievna  
 TITLE OF INVENTION: The Regents of the University of California  
 FILE REFERENCE: 023070-099910US  
 CURRENT APPLICATION NUMBER: US/09/840, 743  
 PRIOR FILING DATE: 2001-04-23  
 PRIOR APPLICATION NUMBER: US 09/553,690  
 NUMBER OF SEQ ID NOS: 119  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 19  
 LENGTH: 12120  
 TYPE: DNA  
 ORGANISM: Oryza sativa  
 FEATURE:  
 OTHER INFORMATION: DMTRICE sequence from PAC P0489G09  
 US-09-840-743-19

Query Match 4.5%; Score 80.4; DB 10; Length 12120;  
 Best Local Similarity 73.4%; Pred. No. 4.6e-09;  
 Matches 116; Conservative 0; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 ACTTAGATAATAAGTAAGTACCAAGAAAATAATAATTCACAAAT-TTTTTTAAT 59  
 DB 11342 ACTGTGAATAATAAGTAAGTACCAAAATAATAATAATTCACAAATTTTTTGAAT 11283

QY 60 AAGACGAGTGGTCAACAGTACAAAGTAAATACTCAAAATTCCTTATATTATGGGACTTAT 119  
 DB 11282 AAGCGAGTGGTCAACAGTTCGAAGCAAAACTCAAAATCTCTTATATTATGGGACGGAG 11223  
 QY 120 ATTATGGACGGAGGAAGTAGAAGATTGTAGCCAGAA 157  
 DB 11222 GGAGTAGCAATTTACCCCTTAAGCAGCTTTCTGCCAACAA 11185

RESULT 6  
 US-10-260-238-2150  
 Sequence 2150, Application US/10260238  
 Publication No. US20040016025A1  
 GENERAL INFORMATION:  
 APPLICANT: Budworth, Paul R.  
 APPLICANT: Moughamer, Todd G.  
 APPLICANT: Briggs, Steven P.  
 APPLICANT: Cooper, Bret  
 APPLICANT: Glazebrook, Jane  
 APPLICANT: Goff, Stephen A.  
 APPLICANT: Katagiri, Fumiya  
 APPLICANT: Kreps, Joel  
 APPLICANT: Provart, Nicholas  
 APPLICANT: Ricke, Darrell  
 APPLICANT: Zhu, Tong  
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
 FILE REFERENCE: 60111-NP  
 CURRENT APPLICATION NUMBER: US/10/260,238  
 PRIOR FILING DATE: 2002-09-26  
 PRIOR APPLICATION NUMBER: US 60/325,448  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: US 60/325,277  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: US 60/370,620  
 PRIOR FILING DATE: 2002-04-04  
 NUMBER OF SEQ ID NOS: 6077  
 SEQ ID NO 2150  
 LENGTH: 2000  
 TYPE: DNA  
 ORGANISM: Oryza sativa  
 US-10-260-238-2150

Query Match 4.5%; Score 80; DB 16; Length 2000;  
 Best Local Similarity 86.2%; Pred. No. 2.3e-09;  
 Matches 100; Conservative 0; Mismatches 15; Indels 1; Gaps 1;  
 QY 1 ACTTTAGATAATAAGTAAGTACCAAGAAAATAATAATTCACAAATTTTTTTTAAT 59  
 DB 352 ACGGTAGATAATAAGTAAGTACCAAAATAATAATAATTCACAAATTTTTTGAAT 411  
 QY 60 AAGACGAGTGGTCAACAGTACAAAGTAAATACTCAAAATTCCTTATATTATGGGAC 115  
 DB 412 AAGACGAGTGGTCAAAATGTTGCAACAAAATACTCAAAATTCCTTATATTATGGGAC 467

RESULT 7  
 US-10-260-238-2454  
 Sequence 2454, Application US/10260238  
 Publication No. US20040016025A1  
 GENERAL INFORMATION:  
 APPLICANT: Budworth, Paul R.  
 APPLICANT: Moughamer, Todd G.  
 APPLICANT: Briggs, Steven P.  
 APPLICANT: Cooper, Bret  
 APPLICANT: Glazebrook, Jane  
 APPLICANT: Goff, Stephen A.  
 APPLICANT: Katagiri, Fumiya  
 APPLICANT: Kreps, Joel  
 APPLICANT: Provart, Nicholas  
 APPLICANT: Ricke, Darrell  
 APPLICANT: Zhu, Tong  
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION



QY	60	AAGACGAGTGGTCAACACAGTCAAGTAAAAATTCCTTATATATGGGAC	115
Db	1507	AAGACGAGTGGTCAACGTTGCAAGCAAAATCCTTATAATCCCTTATATATGGGAC	1452

RESULT 9

US-10-260-238-1664/c

; Sequence 1664, Application US/10260238

; Publication No. US20040016025A1

; GENERAL INFORMATION:

; APPLICANT: Budworth, Paul R.

; APPLICANT: Moughamer, Todd G.

; APPLICANT: Briggs, Steven P.

; APPLICANT: Cooper, Bret

; APPLICANT: Glazebrook, Jane

; APPLICANT: Goff, Stephen A.

; APPLICANT: Katagiri, Fumiya

; APPLICANT: Kreps, Joel

; APPLICANT: Provart, Nicholas

; APPLICANT: Ricke, Darrell

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION

; FILE REFERENCE: 60111-NP

; CURRENT APPLICATION NUMBER: US/10/260,238

; CURRENT FILING DATE: 2002-09-26

; PRIOR APPLICATION NUMBER: US 60/325,448

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 60/325,277

; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: US 60/370,620

; PRIOR FILING DATE: 2002-04-04

; NUMBER OF SEQ ID NOS: 6077

; SEQ ID NO 1664

; LENGTH: 2000

; TYPE: DNA

; ORGANISM: *Oryza sativa*

US-10-260-238-1664

Query Match 4.3%; Score 76.8; DB 16; Length 2000;

Best Local Similarity 84.5%; Pred. No. 1.5e-08;

Matches 98; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY	1	ACTTTAGATTAATAAGTAACTGCACAGAAAAATAATAATTCCAAATTTTTT-AAAT	59
Db	1161	ACTGTGGATTAATAAGTAAGTGCACATAAATAATAATAATTTTAAAAAAATTAAT	1102

QY 60 AAGACGAGTGGTCAACACAGTCAAGTAAAAATTCCTTATATATGGGAC 115

Db 1101 AAGACGAGTCAACACATGTAAGCAAAAACACAAAATTCCTTATATATGGGAC 1046

RESULT 10

US-10-437-963-10006

; Sequence 10006, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 10006

; LENGTH: 6064

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; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16369C.1
US-10-437-963-1006

Query Match
Best Local Similarity 4.2%; Score 75; DB 17; Length 6064;
Matches 104; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGGGAC 58
Db 3210 ACTTTGATAATAAGCAAGTCACAA-AAAAATAATAATTCCTTATATGGGAC 3268
QY 59 TAAGACGAGTGGTCAACAGTACAGTAAACAACTCAAAATTCCTTATATGGGAC 115
Db 3269 TAAGACGAGTAAATCAAGAGTCAACAACTCAAAATTCCTTATATGGGAC 3325

RESULT 11
US-10-260-238-2176
; Sequence 2176, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, FumiYaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricks, Bartell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NF
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2176
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (573)..(573)
; OTHER INFORMATION: n = any nucleotide
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; OTHER INFORMATION: n = any nucleotide
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; NAME/KEY: N region
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; NAME/KEY: N region
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; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (1960)..(1960)
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; LOCATION: (1999)..(1999)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-2176
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Matches 95; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGG 112
Db 1551 ACCGTAGATAATAAGTAAGTCACTCAAAATAATAATAATTCCTTATATGG 1610
QY 60 AAGACGAGTGGTCAACAGTACAGTAAACAACTCAAAATTCCTTATATGG 112
Db 1611 AATACGAGTGCATCAACGTTGTAAGTAAACAACTCAAAATTCCTTATATGG 1663
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RESULT 12
US-10-437-963-50400/c
; Sequence 50400, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 50400
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52890C.1
US-10-437-963-50400
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Matches 94; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1 ACTTTAGATAATAAGTAAGTCACAGAGAAAATAATAATTCCTTATATGG 59
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Db 5014 AAGACAGTGTCTCAACGTTGTAAGTAAACAACTCAAAATTCCTTATATGG 4964
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RESULT 13



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2004, 10:45:20 ; Search time 5094 Seconds  
(without alignments)  
12675.933 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataagtaag.....ctcttctcttcagtgcaag 1772

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	460.6	26.0	493	AB157032	Oryza sat
C 2	148.2	8.4	626	CL552633	OB_Ba009
C 3	131.4	7.4	802	CL549942	OB_Ba008
C 4	99	5.6	609	CL709985	OR_BBa003
C 5	98.2	5.5	663	AQ872280	nbeb0047D
C 6	97.2	5.4	783	CL734947	OR_BBa006
C 7	95.8	5.4	681	CL837854	OR_CBa006
C 8	92.6	5.2	406	CL712255	OR_BBa003
C 9	92.6	5.2	641	CL625050	OR_BBa002
C 10	91	5.1	703	CL725327	OR_BBa005
C 11	90.4	5.1	582	CL788096	OR_BBa010
C 12	90.4	5.1	660	CL826141	OR_CBa004
C 13	90.2	5.1	764	CL795980	OR_CBa000
C 14	89.4	5.0	881	CL732636	OR_BBa006
C 15	88	5.0	566	CL617540	OR_BBa001
C 16	88	5.0	569	AQ272200	nbbx0027L
C 17	88	5.0	643	CL770798	OR_BBa014
C 18	88	5.0	767	CL732306	OR_BBa006
C 19	87.8	5.0	375	CL782567	OR_BBa009
C 20	87.8	5.0	482	CL520455	SAK1G08 F
C 21	87.8	5.0	573	CL743078	OR_BBa007
C 22	87.8	5.0	820	AQ861700	nbeb0017G
C 23	87	4.9	478	CL733727	OR_BBa006
C 24	87	4.9	680	AQ289268	nbbx0034B

C 25	86.8	4.9	606	9	CL744089	OR_BBa008
C 26	86.8	4.9	679	9	CL756822	OR_BBa012
C 27	86.4	4.9	711	9	CL764853	OR_BBa013
C 28	86.4	4.9	835	9	CL776676	OR_BBa009
C 29	86.2	4.9	536	9	CL733616	OR_BBa006
C 30	86.2	4.9	703	9	CL782409	OR_BBa009
C 31	86.2	4.9	728	6	CB663138	OSJNED07M
C 32	86.2	4.9	744	9	CL755341	OR_BBa012
C 33	86.2	4.9	822	9	CL755195	OR_BBa012
C 34	85.8	4.8	744	9	CL817420	OR_CBa003
C 35	84.8	4.8	429	8	AQ509735	nbxb0096J
C 36	84.8	4.8	512	9	CL710177	OR_BBa003
C 37	84.8	4.8	528	9	CL746902	OR_BBa011
C 38	84.8	4.8	556	8	AQ509717	nbxb0096H
C 39	84.8	4.8	633	8	AQ510370	OR_BBa013
C 40	84.8	4.8	879	9	CL762853	OR_BBa013
C 41	84.6	4.8	628	8	AQ157226	nbxb0009K
C 42	84.2	4.8	596	9	CL715023	OR_BBa004
C 43	83.8	4.7	588	9	CL717546	OR_BBa004
C 44	83.8	4.7	700	9	CL841972	OR_CBa007
C 45	83.8	4.7	715	9	CL827638	OR_CBa004

## ALIGNMENTS

AB157032 493 bp DNA linear GSS 23-DEC-2003  
Oryza sativa (japonica cultivar-group) DNA, clone:T27150T, 3',  
flanking sequence of Tos1 insertion in rice strain NG0531, genomic  
survey sequence.

AB157032

AB157032.1 GI:40315745

GSS.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 Miyao,A., Tanaka,K., Murata,K., Sawaki,H., Takeda,S., Abe,K.,

Shinozuka,Y., Onosato,K. and Hirochika,H.

Target site specificity of the Tos1 retrotransposon shows a

preference for insertion within genes and against insertion in

retrotransposon-rich regions of the genome

Plant Cell 15 (8), 1771-1780 (2003)

12897251

2 (bases 1 to 493)

Miyao,A. and Hirochika,H.

Direct Submission

Submitted (19-DEC-2003) Akiyo Miyao, National Institute of

Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai,

Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,

URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,

Fax:81-298-38-7020)

Location/Qualifiers

1. 493

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/strain="NG0531"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="T27150T"

/clone\_lib="PCR product directly amplified from rice

genomic DNA"

/note="The 3' end of retrotransposon Tos1.7 was found

immediately upstream of this sequence."

ORIGIN

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Best Local Similarity 98.4%; Pred. No. 3.5e-105;

Matches 485; Conservative 0; Mismatches 6; Indels 2; Gaps 2;





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FEATURES
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        /lab_host="E. coli DH10B"
        /clone_lib="CUGI Rice BAC Library (EcoRI)"
        /notes="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
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ORIGIN

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Query Match      5.5%; Score 98.2; DB 8; Length 663;
Best Local Similarity 89.1%; Pred. No. 1.5e-13;
Matches 106; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ACTTTAGATTAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 60
Db 200 ACTTTGGATAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 259

Qy 61 AGACGAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 119
Db 260 AGACAAAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 318

RESULT 6
CL734947 783 bp DNA linear GSS 27-JUL-2004
LOCUS OR_BBA0068F07.f OR_BBA Oryza rufipogon genomic clone OR_BBA0068F07
DEFINITION 5', genomic survey sequence.
ACCESSION CL734947
VERSION CL734947.1 GI:50669303
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 783)
Kim.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,
Kudrna.D., Muller.C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
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FEATURES

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        /cultivar="Nipponbare"
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        /lab_host="E. coli DH10B"
        /clone_lib="CUGI Rice BAC Library (EcoRI)"
        /notes="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
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ORIGIN

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Query Match      5.5%; Score 98.2; DB 8; Length 663;
Best Local Similarity 89.1%; Pred. No. 1.5e-13;
Matches 106; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ACTTTAGATTAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 60
Db 200 ACTTTGGATAATAAGTAAGTCACAGAAAATAATAATAATTCCTTATTTTAAATA 259

Qy 61 AGACGAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 119
Db 260 AGACAAAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 318

RESULT 6
CL734947 783 bp DNA linear GSS 27-JUL-2004
LOCUS OR_BBA0068F07.f OR_BBA Oryza rufipogon genomic clone OR_BBA0068F07
DEFINITION 5', genomic survey sequence.
ACCESSION CL734947
VERSION CL734947.1 GI:50669303
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 783)
Kim.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,
Kudrna.D., Muller.C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
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BACKWARD: CAC TCA TTA GGC ACC CCA
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ORIGIN

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Matches 105; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 61 AGACGAGTGGTCAACAGTACAGTAAATACTCAAAATTCCTTATTTATGGGACTTAT 118
Db 381 AGACAAATGTGCAATTAATACAGTAAATACTCAAAATTCCTTATTTATGAATTGA 438

RESULT 7
CL837854 681 bp DNA linear GSS 09-AUG-2004
LOCUS OR_CBA0063G17.r OR_CBA Oryza rufipogon genomic clone OR_CBA0063G17
DEFINITION 3', genomic survey sequence.
ACCESSION CL837854
VERSION CL837854.1 GI:51083464
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 681)
Kim.H., Yu.Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
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    /clone_lib="OR_CBA"
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FEATURES
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        /dev stage="2 week old seedlings"
        /lab_host="DH10B-T1 phage resistant"
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        /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;"
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Kudrina, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.

TITLE  
JOURNAL  
COMMENT

OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: <http://genome.arizona.edu>  
PCR Primers  
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BACKWARD: CAC TCA TTA GGC ACC CCA  
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FEATURES  
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QY 61 AGACGAGTGGTCAACAGTACAACTCAAAATTCCTTATATATATGGGAC 115  
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Db 597 AGACGAATGTTAAACAGTCAAGTAACAACTCAAAATTCCTTATATATAGAAC 543  
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RESULT 11  
CL788096/c  
LOCUS  
DEFINITION OR\_BB0106H03.f OR\_BBa Oryza rufipogon genomic clone OR\_BB0106H03  
5', genomic survey sequence.  
ACCESSION  
VERSION CL788096.1 GI:50867747  
KEYWORDS  
SOURCE  
ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.  
OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: <http://genome.arizona.edu>  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
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FEATURES  
source

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/note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN

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Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Db 255 AGACGAGTGGTCAACCTTGTAAACAAAACCTTAAATCTCTTATATTCGGGCGGATG 196  
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QY 121 TTATGGCAGCGAGGAGTAGAAGATTGT 148  
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Db 195 GAGTGTAGTGTAGTAGTAGTAGTGTGT 168  
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ACCESSION  
VERSION CL826141.1 GI:51071751  
KEYWORDS  
SOURCE  
ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS Kim,H., Yu,Y., Wisotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.  
OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: <http://genome.arizona.edu>  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
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Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

FEATURES  
source

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Enarthroideae; Oryzaceae; Oryza.  
1 (bases 1 to 566)  
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,  
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

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PCR Primers  
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FEATURES  
source

ORIGIN

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Db 530 ACTTTGGATATAAAGTAAGTCACAAAGAAAATAATAACAAATCTAAATTTTTTTAAT 471  
Qy 60 AAGACGAGTGGTCAACAGTACAAAGTAAAACTCAAAATTCCTTATATTATGGGAC 115  
Db 470 AAGCGAATGGTCAACAGTCCAGCAAAACTCAAAATCCCTTATATTATGGAC 415

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